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C07K014/195 C07K014/205 C07K016/12 C12N001/15 C12N001/19 C12N001/21 C12N005/10
 C12N009/80 C12N015/09 C12N015/52 C12N015/55 C12Q001/68 G01N033/15 G01N033/50
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Term	Documents
((1.TI,AB,CLM.) AND 4).PGPB,USPT,USOC,EPAB,JPAB,DWPI.	31
(L4 AND L1.TI,AB,CLM.).PGPB,USPT,USOC,EPAB,JPAB,DWPI.	31

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<u>#27</u> Search several helicobacter ureases	17:22:35	<u>28</u>
<u>#26</u> Search several ureases	17:22:15	<u>118</u>
<u>#25</u> Search isoforms ureases	17:21:17	<u>7</u>
<u>#24</u> Search multiple ureases	17:20:40	<u>4</u>
<u>#23</u> Search helicobacter felis urease subunit y	17:09:52	<u>0</u>
<u>#22</u> Search helicobacter felis urease subunit x	17:09:47	<u>0</u>
<u>#20</u> Search helicobacter felis urease xy	17:09:31	<u>0</u>
<u>#21</u> Search helicobacter felis urexy		

Search notes
11/6/07

FIGURE 1b = မြတ်စွာ ပြန်လည်

11/15/99					
ALIGNED SEQUENCES					
Reference molecule:	ureXCS1	1 -	226	(226 aa)	Homology
Sequence 2:	ureXkuka	1 -	226	(226 aa)	100%
Sequence 3:	ureXDS4	1 -	226	(226 aa)	99%
Sequence 4:	ureX2301	1 -	226	(226 aa)	99%
Sequence 5:	ureX390	1 -	226	(226 aa)	99%
Sequence 6:	A felis	1 -	237	(237 aa)	50%
Sequence 7:	A pylori	1 -	238	(238 aa)	52%
Sequence 8:	A heilmann	1 -	234	(234 aa)	54%

Alignment type: Global Protein Mismatch 2; Open Gap 4; Extend Gap 1; Conserv N
 Parameters: Parameters:

ureXCS1 (1) vkitprkeqekfllyyagevarkrkaeglklnqpeaiayisahimdearrgkktvagliqmeecmhflkkdevmpgvgmmpdlgeatfpdgktlvtnwpiepdehfkagevkfgcdkdie
 ureXkuka (1)
 ureXDS4 (1)
 ureX2301 (1) ?
 ureX390 (1)ld lm h...rl eea1.r.v...yt..v.1...grv.ek...d.n.s.d...q.grtw...en..d...as.ihav.i..n...iht.v.dngklap...-l.kne..t
 A felis (1) m...ld lm h...1.k...ek.i...yy..v.1...e...a...a.e...q.grtl..p.d..d...as.ihav.i..n...iht.v.agsdkl.pgevilkne..t
 A pylori (1) m...ld lm h...1.kq...k.i...yt..v.1...v.e...a...s.d...q.grtl..a.d...ah.ihav.i..g...iht.v.agsdkl.pgevilkne..t
 A heilmann (1) m...ld lm h...1.kq...k.i...yt..v.1...v.e...a...s.d...q.grtl..a.d...ah.ihav.i..g...iht.v.agsdkl.pgevilkne..t
 ureXCS1 (121) lnagkevtalevtneaspkslnvgshfhfffeankalkfdrakeygrkldipsqntirigaggtrkvqliplgsskkvqglmgnlvnniaderhkhkaldkakshgfi-k
 ureXkuka (121)
 ureXDS4 (121)
 ureX2301 (121)t.
 ureX390 (121) v...ais.k.k.k.drpvq...t.
 A felis (120) i...kavsvk.k.v.drpvq1...v.l.d...a.sfc...v.l.d...a.sfc...a.tav.fep.eeks.e.di...n.rif.f.a..drq..nes.ki..hr...er...ngaksddnyvktike
 A pylori (120) i.e...kavsvk.k.v.drpvq1...v.rc.d...v.l.d...a.tav.fep.eeks.e.di...n.rif.f.a..drq..nes.ki..hr...er...ngaksddnyvktike
 A heilmann (121)havq.k.k.drpvq...v.l.d...a.tav.fep.eeks.e.di...n.rif.f.a..drq..nes.ki..hr...er...ngaksddnyvktike

Figure 1b